

re-run

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/767,561

Source: 1 FWO

Date Processed by STIC: 8/31/04

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 03/07/2005

PATENT APPLICATION: US/10/767,561

TIME: 15:24:12

Input Set : N:\Crf4\Refhold\10\_folder\J767561.raw

Output Set: N:\CRF4\03072005\J767561.raw

## SEQUENCE LISTING

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1 (1) GENERAL INFORMATION:
2     (i) APPLICANT: Freeman, Gordon J.
3         Nadler, Lee M.
4         Gray, Gary S.
5     (ii) TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3
6         WITH INCREASED IMMUNOGENICITY AND USES THEREFOR
7     (iii) NUMBER OF SEQUENCES: 8
8     (iv) CORRESPONDENCE ADDRESS:
9         (A) ADDRESSEE: LAHIVE & COCKFIELD
10        (B) STREET: 60 State Street, Suite 510
11        (C) CITY: Boston
12        (D) STATE: Massachusetts
13        (E) COUNTRY: USA
14        (F) ZIP: 02109
15    (v) COMPUTER READABLE FORM:
16        (A) MEDIUM TYPE: Floppy disk
17        (B) COMPUTER: IBM PC compatible
18        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
19        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
20    (vi) CURRENT APPLICATION DATA:
C--> 21        (A) APPLICATION NUMBER: US/10/767,561
C--> 22        (B) FILING DATE: 28-Jan-2004
23        (C) CLASSIFICATION:
24    (vii) PRIOR APPLICATION DATA:
W--> 25        (A) APPLICATION NUMBER: US/09/206,132
26        (B) FILING DATE: 07-DEC-1998
W--> 27        (A) APPLICATION NUMBER: 08/456,104
28        (B) FILING DATE:
W--> 29        (A) APPLICATION NUMBER: 08/101,624
30        (B) FILING DATE: 26-JUL-1993
W--> 31        (A) APPLICATION NUMBER: 08/109,393
32        (B) FILING DATE: 19-AUG-1993
33    (viii) ATTORNEY/AGENT INFORMATION:
34        (A) NAME: Mandragouras, Amy E.
35        (B) REGISTRATION NUMBER: 36,207
36        (C) REFERENCE/DOCKET NUMBER: RPI-008
37    (ix) TELECOMMUNICATION INFORMATION:
38        (A) TELEPHONE: (617) 227-7400
39        (B) TELEFAX: (617) 227-5941
40 (2) INFORMATION FOR SEQ ID NO: 1:
41     (i) SEQUENCE CHARACTERISTICS:
42     (A) LENGTH: 1120 base pairs

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43      (B) TYPE: nucleic acid
44      (C) STRANDEDNESS: single
45      (D) TOPOLOGY: linear
46      (ii) MOLECULE TYPE: cDNA
47      (ix) FEATURE:
48          (A) NAME/KEY: CDS
49          (B) LOCATION: 107..1093
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT      60
52 GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC      115
53                                     Met Asp Pro
54                                     1
55 CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG      163
56 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
57      5      10      15
58 CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT      211
59 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
60      20      25      30      35
61 GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT      259
62 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
63      40      45      50
64 GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG      307
65 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
66      55      60      65
67 GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG      355
68 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
69      70      75      80
70 GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT      403
71 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
72      85      90      95
73 CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA      451
74 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
75      100      105      110      115
76 AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA      499
77 Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
78      120      125      130
79 GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA      547
80 Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
81      135      140      145
82 ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC      595
83 Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr
84      150      155      160
85 CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT      643
86 Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr
87      165      170      175
88 ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA      691
89 Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu
90      180      185      190      195
91 CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG      739

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92 Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr
93          200          205          210
94 AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT      787
95 Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu
96          215          220          225
97 TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA      835
98 Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro
99          230          235          240
100 GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT      883
101 Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys
102          245          250          255
103 GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG      931
104 Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg
105 260          265          270          275
106 CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG      979
107 Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu
108          280          285          290
109 AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT      1027
110 Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser
111          295          300          305
112 GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC      1075
113 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp
114          310          315          320
115 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA      1120
116 Lys Ser Asp Thr Cys Phe
117          325
119 (2) INFORMATION FOR SEQ ID NO: 2:
120 (i) SEQUENCE CHARACTERISTICS:
121 (A) LENGTH: 329 amino acids
122 (B) TYPE: amino acid
123 (D) TOPOLOGY: linear
124 (ii) MOLECULE TYPE: protein
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
126 Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
127 1          5          10          15
128 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
129          20          25          30
130 Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
131          35          40          45
132 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
133          50          55          60
134 Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
135 65          70          75          80
136 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
137          85          90          95
138 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
139          100          105          110
140 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
141          115          120          125

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142 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
143      130                      135                      140
144 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 145                      150                      155                      160
146 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
147                      165                      170                      175
148 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
149                      180                      185                      190
150 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
151                      195                      200                      205
152 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
153      210                      215                      220
154 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
155 225                      230                      235                      240
156 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
157                      245                      250                      255
158 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
159                      260                      265                      270
160 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
161      275                      280                      285
162 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
163      290                      295                      300
164 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
165 305                      310                      315                      320
166 Ser Cys Asp Lys Ser Asp Thr Cys Phe
167                      325

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169 (2) INFORMATION FOR SEQ ID NO: 3:

170 (i) SEQUENCE CHARACTERISTICS:

171 (A) LENGTH: 1151 base pairs

172 (B) TYPE: nucleic acid

173 (C) STRANDEDNESS: double

174 (D) TOPOLOGY: linear

175 (ii) MOLECULE TYPE: cDNA

176 (ix) FEATURE:

177 (A) NAME/KEY: CDS

178 (B) LOCATION: 99..1028

179 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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180 GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT      60
181 CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC                      104
182                               Met Asp
183                               1
184 CCC AGA TGC ACC ATG GGC TTG GCA ATC CTT ATC TTT GTG ACA GTC TTG      152
185 Pro Arg Cys Thr Met Gly Leu Ala Ile Leu Ile Phe Val Thr Val Leu
186      5                      10                      15
187 CTG ATC TCA GAT GCT GTT TCC GTG GAG ACG CAA GCT TAT TTC AAT GGG      200
188 Leu Ile Ser Asp Ala Val Ser Val Glu Thr Gln Ala Tyr Phe Asn Gly
189      20                      25                      30
190 ACT GCA TAT CTG CCG TGC CCA TTT ACA AAG GCT CAA AAC ATA AGC CTG      248
191 Thr Ala Tyr Leu Pro Cys Pro Phe Thr Lys Ala Gln Asn Ile Ser Leu

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192	35				40				45				50				
193	AGT	GAG	CTG	GTA	GTA	TTT	TGG	CAG	GAC	CAG	CAA	AAG	TTG	GTT	CTG	TAC	296
194	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Gln	Lys	Leu	Val	Leu	Tyr	
195					55				60				65				
196	GAG	CAC	TAT	TTG	GGC	ACA	GAG	AAA	CTT	GAT	AGT	GTG	AAT	GCC	AAG	TAC	344
197	Glu	His	Tyr	Leu	Gly	Thr	Glu	Lys	Leu	Asp	Ser	Val	Asn	Ala	Lys	Tyr	
198				70					75				80				
199	CTG	GGC	CGC	ACG	AGC	TTT	GAC	AGG	AAC	AAC	TGG	ACT	CTA	CGA	CTT	CAC	392
200	Leu	Gly	Arg	Thr	Ser	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	Leu	His	
201			85					90					95				
202	AAT	GTT	CAG	ATC	AAG	GAC	ATG	GGC	TCG	TAT	GAT	TGT	TTT	ATA	CAA	AAA	440
203	Asn	Val	Gln	Ile	Lys	Asp	Met	Gly	Ser	Tyr	Asp	Cys	Phe	Ile	Gln	Lys	
204		100					105				110						
205	AAG	CCA	CCC	ACA	GGA	TCA	ATT	ATC	CTC	CAA	CAG	ACA	TTA	ACA	GAA	CTG	488
206	Lys	Pro	Pro	Thr	Gly	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr	Glu	Leu	
207	115				120				125				130				
208	TCA	GTG	ATC	GCC	AAC	TTC	AGT	GAA	CCT	GAA	ATA	AAA	CTG	GCT	CAG	AAT	536
209	Ser	Val	Ile	Ala	Asn	Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala	Gln	Asn	
210				135					140				145				
211	GTA	ACA	GGA	AAT	TCT	GGC	ATA	AAT	TTG	ACC	TGC	ACG	TCT	AAG	CAA	GGT	584
212	Val	Thr	Gly	Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	Gln	Gly	
213			150					155				160					
214	CAC	CCG	AAA	CCT	AAG	AAG	ATG	TAT	TTT	CTG	ATA	ACT	AAT	TCA	ACT	AAT	632
215	His	Pro	Lys	Pro	Lys	Lys	Met	Tyr	Phe	Leu	Ile	Thr	Asn	Ser	Thr	Asn	
216		165					170				175						
217	GAG	TAT	GGT	GAT	AAC	ATG	CAG	ATA	TCA	CAA	GAT	AAT	GTC	ACA	GAA	CTG	680
218	Glu	Tyr	Gly	Asp	Asn	Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	
219		180					185				190						
220	TTC	AGT	ATC	TCC	AAC	AGC	CTC	TCT	CTT	TCA	TTC	CCG	GAT	GGT	GTG	TGG	728
221	Phe	Ser	Ile	Ser	Asn	Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asp	Gly	Val	Trp	
222	195				200				205				210				
223	CAT	ATG	ACC	GTT	GTG	TGT	GTT	CTG	GAA	ACG	GAG	TCA	ATG	AAG	ATT	TCC	776
224	His	Met	Thr	Val	Val	Cys	Val	Leu	Glu	Thr	Glu	Ser	Met	Lys	Ile	Ser	
225				215					220				225				
226	TCC	AAA	CCT	CTC	AAT	TTC	ACT	CAA	GAG	TTT	CCA	TCT	CCT	CAA	ACG	TAT	824
227	Ser	Lys	Pro	Leu	Asn	Phe	Thr	Gln	Glu	Phe	Pro	Ser	Pro	Gln	Thr	Tyr	
228			230					235				240					
229	TGG	AAG	GAG	ATT	ACA	GCT	TCA	GTT	ACT	GTG	GCC	CTC	CTC	CTT	GTG	ATG	872
230	Trp	Lys	Glu	Ile	Thr	Ala	Ser	Val	Thr	Val	Ala	Leu	Leu	Leu	Val	Met	
231		245					250				255						
232	CTG	CTC	ATC	ATT	GTA	TGT	CAC	AAG	AAG	CCG	AAT	CAG	CCT	AGC	AGG	CCC	920
233	Leu	Leu	Ile	Ile	Val	Cys	His	Lys	Lys	Pro	Asn	Gln	Pro	Ser	Arg	Pro	
234		260					265				270						
235	AGC	AAC	ACA	GCC	TCT	AAG	TTA	GAG	CGG	GAT	AGT	AAC	GCT	GAC	AGA	GAG	968
236	Ser	Asn	Thr	Ala	Ser	Lys	Leu	Glu	Arg	Asp	Ser	Asn	Ala	Asp	Arg	Glu	
237	275				280				285				290				
238	ACT	ATC	AAC	CTG	AAG	GAA	CTT	GAA	CCC	CAA	ATT	GCT	TCA	GCA	AAA	CCA	1016
239	Thr	Ile	Asn	Leu	Lys	Glu	Leu	Glu	Pro	Gln	Ile	Ala	Ser	Ala	Lys	Pro	
240				295				300				305					

## VERIFICATION SUMMARY

DATE: 03/07/2005

PATENT APPLICATION: US/10/767,561

TIME: 15:24:13

Input Set : N:\Crf4\Refhold\10\_folder\J767561.raw

Output Set: N:\CRF4\03072005\J767561.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:27 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)  
L:29 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)  
L:31 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1)(vii)  
L:441 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7  
L:444 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7